

Effects of Crossing Two Japanese-Quail-Lines Selected Seven Generation for Meat or Egg Production on Growth Traits

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Abstract

Data on a total of 1779 birds, consists of 1273 straight-bred and 506 cross-bred, produced from two Japanese quail lines selected for different production purposes (Meat line, M and Egg line, E) as well as their reciprocal crosses. The study aimed at the evaluation of the heterotic and crossbreeding effects (i.e. additive direct and maternal) for growth traits (i.e. biweekly body weight, BW; growth rate, GR and gain in weight, GW) from hatch up to 6 weeks of age.

Tests of significance revealed that mating group (MG) affect significantly the majority of the studied growth traits except GR during 4-6 wk. Significant differences among (hatch-sex) combination (HS) were obtained except that for BW at 6 wk. Breed of sire (BrS) and dam (BrD) failed to prove any significance on all growth traits investigated except that for BrD on BW at hatch and BrS on GW during 2-4 and GR during 2-4 and 2-6 wks. However, (BrS X BrD) interaction contributed highly significant to variability of most studied traits excluding GW during 4-6 and GR during 2-6 weeks of age. Howbeit, (MG X HS) interaction affected significantly most studied traits aside from BW at 6 wks of age.

Direct heterosis was highly significant for the majority of growth traits though generally negative except that for GR during 4-6 wks of age, which was significantly positive. Direct and maternal additive were almost insignificant on these traits disregard negative direct additive (in favor of egg-type line) GW during 2-4 and GR during 2-4 and 2-6 wks; as well as the positive GR (in favor of meat-type line) maternal effect.

It could be recommended from browsing the crossbreeding outputs that the use of M and E lines still needs some reciprocal recurrent selection effort to achieve a goal of using them to improve the growth traits under consideration.

(Key Words: Japanese quail, growth traits, sexual maturity, heterosis, direct and maternal additive.)

Introduction

Though much of the genetic improvement can be achieved through straight-bred selection (Rishell, 1997), considerable amount of heterosis can also be achieved through crossing. Crossing (Marks, 1995), which is the second major method of exploiting genetic variations of quantitative characters, can be broadly defined as the mating of individuals from different populations and not only between inbred lines. The main purposes of crossing are to produce premium crosses (i.e. make use of hybrid vigor), to improve fitness and fertility traits and to combine different characteristics in which the crossed breeds are meritorious, Willham and Pollak (1985). The genetic backgrounds of populations exploited and involved in the crossbreeding scheme have a vital role at the time of expression and magnitude of heterosis of a given trait. Diversity generated among lines unlikely selected for different characteristics may result in greater non-additive genetic interaction.

Non-additive genetic effect is an important crux in meat and laying stock industries, because of opportunities to combine stocks that complement each other or interact favourably. This allows development of mating combinations for rapid growth yield and other important economic traits (Marks, 1995). In poultry, crossing of populations predominates the commercial industry. However under Egyptian conditions, there is somewhat non-sufficient current data regarding the expression of heterosis for growth traits following short-term selection for increased body weight and/or egg production traits. Because of recent developments in specific product amalgamates (i.e. fast food and yield packages), specific characteristics of parental lines are increasingly important, to launch specific commercial goals. Diversity generated and established among lines selected for different characteristics or under different environments, may possibly result in a greater non-additive genetic interaction in crosses originating from them.

Judging from X^2 values, results of Chrenek *et al.*, 1998 showed that none of the linear models used from different approaches to estimate crossbreeding effects, fitted well. They attributed the using of linear models in this respect, only because they can easily be handled, though there is no reason to assume that nature prefers linear models. As genes act through biochemical and biological processes, non-linearity should be the rule and the question is to what extent this non-linearity can be approximated by linear models. Furthermore, the linear model adopted for the estimation of the genetic group means did not contain the genotype X environment interaction which might be of impact as well. Also models of Dickerson (1992) does not contemplate the various kinds of epistatic effects as parts from the non-additive genetic effects.

The aim of the present study was to estimate crossbreeding effects (*i.e.* mating group, maternal additive, direct additive, breed of sire and breed of dam) for growth traits of two subpopulation of Japanese quail (*i.e.* Meat, M and Egg, E lines) and to estimate the impact of dominance effect (direct heterotic effects) as well as non-genetic effect (hatch X sex).

Materials and Methods

This experiment was carried out at Poultry Research Unit farm, Poultry Production Dept., Faculty of Agriculture at Kafr El-Sheikh, Tanta Univ., Egypt.

Data were obtained on a total number of 1779 Japanese quail birds of straight-bred (1273) and cross-bred (506), produced from two selected lines (Meat production line, M and Egg production line, E) as well as their reciprocal crosses. This gave rise to a total of four mating groups (*i.e.* M x M; E x E; M x E and E x M). The M line was originated from using a seven-generations-selection-index which depends on three traits (growth rate, %; keel and shank lengths, cm. at 28 days), produced from 94 females and 47 males (paired mating system). The E line was instigated from using a parallel seven-generations-selection-index which depends on age at sexual maturity (days) and the period needed to produce the first 10 eggs, produced from 92 females and 46 males (Tawfeek 2001). All the four mating groups of the three hatches were placed in similarly equipped contract production units, with the same management and nutrition regimens (NRC, 1994) in commercial practice at the time of the study. Feed and water were provided *ad libitum*. The used corn-soyabean diet contained 28% crude protein and 3100 kcal ME till 14 days of age followed by 25% crude protein and 2900 kcal ME till 42 days. Hatched chicks were wing banded and brooded in floor brooders. Weights were recorded to the nearest gram at hatch, 1, 2 and 6 weeks of age and gain in weight along

with growth rate percentages relative to mean of the two subsequent weights of each period, were calculated. Birds were sexed at 4 wks of age according to plumage pattern and color. Those birds alive to the end of the experimental period and with known sex are included in the analysis. The index of genetic distance (D) was calculated, by sex, hatch and (sex X hatch) interaction for growth traits as explained by (Nei, 1978 and Hartl and Clark, 1989). The equation used is $D = -\ln \{ [0.5 * (\mu_{ME} + \mu_{EM})] / [0.5 * (\mu_{MM} + \mu_{EE})] \}$ where: μ_{ME} ; μ_{EM} ; μ_{MM} and μ_{EE} are arithmetic means of individual values of the two reciprocal and two straightbred mating groups for a given growth trait.

Mixed model Least Squares and Maximum Likelihood Computer Program PC version 2, LSMLMW (Harvey, 1990) was used for analyzing the data. Significance levels are reported at the $P \leq 0.05$ level. The linear fixed model adopted for the analysis comprised the effects of mating groups, MG (4 classes); hatch effect, H (3 classes); as well as the interactions between MG x H. The basic form of the general linear mathematical model is:

$$Y = X\beta + e \quad \text{Where;}$$

Y = an observational column vector of Japanese quail growth records of i trait.

X = Incidence matrix of zeros and ones which relating records to the appropriate fixed effects for a given trait i.

β = the vector of unknown fixed effects for trait i.

e = The vector of random residual effect for trait i.

The method of least squares analysis (*i.e.* using the residual error mean squares) was used for parameter estimation (Chrenek *et al.*, 1998). In a general form, the expected value can be written for any genetic group as follows (reported by Wolf *et al.*, 1995):

$$G' = \mu + (\alpha_1 - \alpha_2) g + \delta_{12} h + (\alpha_1^M - \alpha_2^M) a^M$$

Where:

G' = Least squares mean of the given genetic group G;

μ = General Least squares mean ("genetic background", reference value for remaining genetic effects);

α_i = proportion of genes in G from the *i*th source population ($i = 1, 2$);

g = direct additive effect (sire breed difference);

δ_{ij} = probability that at a randomly chosen locus of a randomly chosen individual of G one allele is from the *i*th (*i*th) source population and the other is from the *j*th (*i*th) source population ($i, j = 1, 2$ and $i \leq j$);

h = direct heterotic effect and it includes part of the additive X additive interaction;

α_i^M = proportion of genes in the dam population of G from the i th source population ($i = 1, 2$);

a^M = maternal additive effect

Crossbreeding effects (direct additive G_i ; maternal Additive G_m ; direct heterotic H^1 effects) on different traits were derived applying a selected set of linear contrasts on mating groups' least squares means (Dickerson, 1992). The genetic model applied for the estimation of these effects was as follows:

Contrast	Genotypes†				Divisor
	M x M	E x E	M x E	E x M	
Straight-bred difference	1	-1	0	0	1
Direct heterotic	-1	-1	1	1	2
Individual or directional (Separate cross) heterosis:					
M x E	-1	-1	2	0	2
E x M	-1	-1	0	2	2
Direct additive	1	-1	1	-1	1
Maternal additive	0	0	-1	1	1

† Sire strain is denoted first and dam strain second.

M = Meat line; E = Egg line.

Results and Discussion

Means and coefficient of variations of uncorrected records:

Means (μ), standard error (\pm SE), number of observations (n) and coefficient of variation (CV%) for every mating groups (MG) peculiar to biweekly growth (*i.e.* body weight, BW; gain in weight, GW and growth rate, GR) traits for age periods from hatch till six weeks of age are presented in table 1.

However, a general trend could be detected concerning CV% for different growth traits revealing that CV% of crosses were somewhat higher compared to pures (Table 1) indicating that crossing had unexpectedly increased the variability between crossbred individuals. Though it is known that selection acts in increasing homogeneity within the considered loci as inbreeding but since the selection is not for the same loci, such action is not definitely evident.

Apart from the miscellaneous mating groups (*i.e.* Focusing on overall, lines and crosses means) and with regard to equally spaced age periods in case of GW and GR (*i.e.* 0-2, 2-4 and 4-6 wk). There was a general trend for CV% of growth rate that its percentage of phenotypic variability tended to amplify as age or weight of quails increased. However, a fluctuated trend was observed when considering GW. Body weight phenotypic variation of all groups at the 2nd weeks of age was exceptionally at incomparable rise to that in other ages, which in turn has its consequences on gain in weight at 2-4 weeks of age (Table 1).

However, higher phenotypic variations in later

ages than that at earlier ones could be ascribed to the consequence of the combination of nongenetic and genetic factors (Tawfeek, 1995).

Mating group (MG):

Highly significant differences ($P \leq 0.0001$; $P \leq 0.001$ or $P \leq 0.01$; Table 2) for the effect of MG on growth traits, except GW during 4-6 weeks of age were detected. Similarly, Sabra (1990), Bahie El-Deen *et al.*, (1998) and Nofal *et al.*, (2003) reported that differences among pure lines and their crosses for growth traits were significant.

Straight-breds generally acquired heavier least squares means of BW along with higher GW and GR compared to the crossbred ones (Table 3). Meat line got insignificantly (except at hatch; $P \leq 0.05$; Tables 4&5) higher BW than egg line, while egg line quails attained superiority in GR at most age periods considered, (Table 4) with significance detected only at 2-4 and 2-6 weeks of age ($P \leq 0.05$ $P \leq 0.01$; respectively; table 5). However, no detectable trend for straight-bred differences in GW could be detected.

Crosses sired by egg line were somewhat higher in BW and GR of most age periods considered; table 3 with this tendency to be less clear in case of GW.

Hatch-Sex combinations (HS):

Significant differences ($P \leq 0.0001$; $P \leq 0.001$ or $P \leq 0.05$) were found among HS groups for all growth traits except BW at 6 weeks of age, (Table 2).

Data of Least-squares means for different growth traits given in table 3, revealed that females

Table 1: Number of observations (n), actual means (μ), standard errors (\pm SE) and coefficients of variation (CV%) of various mating groups regarding body weight (BW), gain in weight (GW) and Growth rate (GR) traits from hatch till 6 weeks of age.

Trait & Mating groups		Body weight (BW) / Age per weeks					
		At hatch	2 wks	4 wks	6 wks		
Overall Mean	$\mu \pm$ SE	8.49 \pm 0.01	56.79 \pm 0.20	102.27 \pm 0.25	146.07 \pm 0.44		
n = 1779	CV%	4.45	14.89	10.22	12.65		
Straight-Bred:							
Meat line (M)	$\mu \pm$ SE	8.55 \pm 0.02	57.74 \pm 0.33	104.02 \pm 0.38	147.94 \pm 0.71		
n = 632	CV%	4.60	14.29	9.22	12.02		
Egg line (E)	$\mu \pm$ SE	8.51 \pm 0.01	56.90 \pm 0.32	103.55 \pm 0.38	147.61 \pm 0.69		
n = 641	CV%	4.10	14.05	9.41	11.87		
Overall (Lines)	$\mu \pm$ SE	8.52 \pm 0.01	57.32 \pm 0.23	103.78 \pm 0.27	147.78 \pm 0.49		
n = 1273	CV%	4.36	14.19	9.31	11.94		
Cross-Bred:							
M X E	$\mu \pm$ SE	8.38 \pm 0.02	55.57 \pm 0.55	98.21 \pm 0.70	141.12 \pm 1.26		
n = 263	CV%	4.37	15.94	11.55	14.51		
E X M	$\mu \pm$ SE	8.44 \pm 0.02	55.36 \pm 0.60	98.76 \pm 0.74	142.46 \pm 1.22		
n = 243	CV%	4.44	16.89	11.62	13.37		
Overall (Crosses)	$\mu \pm$ SE	8.41 \pm 0.02	55.47 \pm 0.40	98.48 \pm 0.51	141.76 \pm 0.88		
n = 506	CV%	4.52	16.39	11.56	13.96		
Trait & Mating groups		Gain in weight (GW) / Age period per weeks					
		0-2	0-4	0-6	2-4	2-6	4-6
Overall Mean	$\mu \pm$ SE	48.30 \pm 0.19	93.78 \pm 0.24	137.57 \pm 0.43	45.48 \pm 0.13	89.27 \pm 0.30	43.79 \pm 0.25
n = 1779	CV%	16.96	10.90	13.30	12.06	14.13	24.41
Straight-Bred:							
Meat line (M)	$\mu \pm$ SE	49.20 \pm 0.32	95.47 \pm 0.37	139.39 \pm 0.70	46.28 \pm 0.20	90.20 \pm 0.50	43.93 \pm 0.43
n = 632	CV%	16.23	9.81	12.61	10.81	13.82	24.73
Egg line (E)	$\mu \pm$ SE	48.39 \pm 0.31	95.04 \pm 0.38	139.11 \pm 0.68	46.64 \pm 0.21	90.71 \pm 0.47	44.07 \pm 0.40
n = 641	CV%	16.03	10.03	12.45	11.52	13.15	22.87
Overall (Lines)	$\mu \pm$ SE	48.79 \pm 0.22	95.26 \pm 0.26	139.25 \pm 0.49	46.46 \pm 0.15	90.46 \pm 0.34	43.99 \pm 0.29
n = 1273	CV%	16.15	9.92	12.52	11.18	13.48	23.80
Cross-Bred:							
M X E	$\mu \pm$ SE	47.19 \pm 0.53	89.83 \pm 0.68	132.74 \pm 1.25	42.64 \pm 0.35	85.55 \pm 0.89	42.91 \pm 0.78
n = 263	CV%	18.23	12.32	15.26	13.40	14.13	29.46
E X M	$\mu \pm$ SE	46.91 \pm 0.58	90.32 \pm 0.72	134.02 \pm 1.20	43.40 \pm 0.33	87.16 \pm 0.74	43.70 \pm 0.61
n = 243	CV%	19.30	12.41	14.01	11.68	13.21	21.62
Overall (Crosses)	$\mu \pm$ SE	47.06 \pm 0.39	90.06 \pm 0.49	133.35 \pm 0.87	43.01 \pm 0.24	86.30 \pm 0.59	43.29 \pm 0.50
n = 506	CV%	18.73	12.36	14.66	12.61	15.25	25.92
Trait & Mating groups		Growth rate (GR) / Age period per weeks					
		0-2	0-4	0-6	2-4	2-6	4-6
Overall Mean	$\mu \pm$ SE	73.62 \pm 0.07	84.55 \pm 0.03	88.88 \pm 0.03	28.80 \pm 0.09	44.06 \pm 0.05	17.49 \pm 0.07
n = 1779	CV%	3.85	1.59	1.34	12.71	7.79	17.07
Straight-Bred:							
Meat line (M)	$\mu \pm$ SE	73.88 \pm 0.11	84.72 \pm 0.05	88.96 \pm 0.05	28.83 \pm 0.14	43.96 \pm 0.14	17.27 \pm 0.12
n = 632	CV%	3.72	1.47	1.30	12.64	8.06	17.50
Egg line (E)	$\mu \pm$ SE	73.68 \pm 0.10	84.72 \pm 0.05	88.98 \pm 0.05	29.26 \pm 0.14	44.39 \pm 0.13	17.40 \pm 0.11
n = 641	CV%	3.57	1.50	1.30	12.28	7.31	16.41
Overall (Lines)	$\mu \pm$ SE	73.78 \pm 0.08	84.72 \pm 0.04	88.97 \pm 0.03	29.05 \pm 0.10	44.19 \pm 0.10	17.34 \pm 0.08
n = 1273	CV%	3.64	1.48	1.30	12.47	7.71	16.95
Cross-Bred:							
M X E	$\mu \pm$ SE	73.37 \pm 0.19	84.13 \pm 0.09	88.62 \pm 0.08	27.96 \pm 0.23	43.51 \pm 0.24	17.74 \pm 0.22
n = 263	CV%	4.27	1.76	1.47	13.44	8.77	19.76
E X M	$\mu \pm$ SE	73.07 \pm 0.20	84.10 \pm 0.09	88.67 \pm 0.08	28.44 \pm 0.23	44.18 \pm 0.20	18.01 \pm 0.16
n = 243	CV%	4.31	1.72	1.33	12.64	6.98	19.76
Overall (Crosses)	$\mu \pm$ SE	73.22 \pm 0.14	84.12 \pm 0.06	88.64 \pm 0.06	27.96 \pm 0.16	44.30 \pm 0.59	17.87 \pm 0.14
n = 506	CV%	4.29	1.74	1.41	13.07	7.97	17.18

Table (2): F-values of least squares analysis of variance of various factors affecting body weight, g. (BW), gain in weight, g. (GW) and Growth rate, % (GR) of Japanese Quail from hatch till 6 weeks of age.

Source of Variations	df	Body weight (BW) / Age per week.					
		At hatch	2 wk.	4 wk.	6 wk.		
Mating Group (MG)	3	15.58****	9.67****	39.57***	16.98****		
Breed of Sire (BS)	1	0.22 ns	1.25 ns	0.10 ns	0.54 ns		
Breed of Dam (BD)	1	7.61**	0.64 ns	1.32 ns	0.83 ns		
BS X BD	1	36.59****	22.99****	113.61****	47.90****		
Hatch X Sex Combination (HS)	5	6.55****	16.90***	21.22****	25.03 ns		
MG X HS	15	1.19 ns	1.98*	1.61 ns	1.62 ns		
Remainder Mean squares	1755	0.136	65.661	95.866	303.809		
R-Squared		0.060	0.093	0.134	0.122		
Source of Variations	df	Gain in weight (GW) / periods (wk).					
		0-2	0-4	0-6	2-4	2-6	4-6
Mating Group (MG)	3	9.22***	39.56****	16.71****	54.06****	16.71****	1.18 ns
Breed of Sire (BS)	1	1.38 ns	0.09 ns	0.54 ns	5.45*	3.32 ns	0.89 ns
Breed of Dam (BD)	1	0.49 ns	1.14 ns	0.75 ns	0.83 ns	0.61 ns	0.20 ns
BS X BD	1	21.77****	113.79****	47.29****	157.50****	46.28****	2.49 ns
Hatch X Sex Combination (HS)	5	17.14****	21.32****	25.14****	7.44****	20.96****	17.19****
MG X HS	15	2.06**	1.65 ns	1.64 ns	1.47 ns	1.38 ns	1.72*
Remainder Mean squares	1755	61.603	91.671	296.467	27.106	144.582	106.362
R-Squared		0.094	0.135	0.122	0.110	0.103	0.081
Source of Variations	df	Growth rate (%) / periods (wk).					
		0-2	0-4	0-6	2-4	2-6	4-6
Mating Group (MG)	3	8.23****	29.53****	11.94****	7.59***	4.66**	4.13**
Breed of Sire (BS)	1	2.23 ns	0.14 ns	0.77 ns	6.13*	10.53**	1.58 ns
Breed of Dam (BD)	1	0.05 ns	0.00 ns	0.04 ns	0.06 ns	0.13 ns	0.03 ns
BS X BD	1	19.40****	86.71****	34.02****	16.81****	2.08 ns	10.95***
Hatch X Sex Combination (HS)	5	18.62****	16.75****	22.19****	4.89***	2.33*	6.91****
MG X HS	15	2.68***	2.04*	1.82 ns	2.05**	1.83*	1.86*
Remainder Mean squares	1755	7.341	1.640	1.286	12.829	11.614	8.549
R-Squared		0.098	0.107	0.106	0.055	0.026	0.053

ns = not significant at $P \leq 0.05$; * significant at $P \leq 0.05$; ** significant at $P \leq 0.01$; *** significant at $P \leq 0.001$; **** significant at $P < 0.0001$.

of the 2nd hatch showed generally the highest growth trait figures in most cases. Nonetheless, in all hatches females were generally heavier in BW and superior to males in GW and GR. As regard to sex effect Minvielle *et al.*, (2000), El-Full (2001) and El-Haleek (2002) reported that sex effect on quail lines was significant with a tendency of females to be heavier at most ages considered. Caron *et al.*, 1990 reported that females grew faster and yielded larger muscles than males at juvenile ages (prematurity). This sex dimorphism could be attributed to an acceleration of weight gain by females prior to laying the first egg Sheble *et al.*, (1996).

Straight-bred differences:

Results of linear contrasts (Table 5) revealed that there was inconsistent trend of superiority ranking for M in BW traits and significantly ($P \leq 0.05$) at hatch. The trend was generally reversed in favor of E line in case of GR but significantly ($P \leq 0.05$ or $P \leq 0.01$) during 2-4 and 2-6 weeks of age. However, no detectable trend or significance could be observed for the straight-bred differences in case of GW. These results showed that selection for differed production purposes appeared to be hardly effective in improving variability of BW in Japanese quail. Similar results were reported by Anthony *et al.*, (1996) when they studied the effect of selection on reproductive performance and effects of selection age on growth response. This relatively low and inclusive discrimination between the lines selected in this population of Japanese quail could be due to the previous selection of BW it had been subjected for. This previous selection could probably consumed a large proportion of the additive genetic variance. Another explanation for this low variability of selected lines in growth traits is that environmental circumstances and feeding regimen applied may not quite sufficient to make the selected lines exhibit and unveil their genetic peculiarities. These genetic peculiarities may influence nutrient requirement and necessitate different constitution of the feeds proposed.

Disconnectedly, Marks (1996) concluded that additive genetic effect is intensely important for BW of quails. In addition, El-Shanty *et al.*, (2001) used three German medium-type strains of chicken (Barnevelder, Mechelner and Italiener) and showed that differences among strains at 16 and 20 weeks of age concerning growth traits of males, were significant. Results of significant effect of Japanese Quail strain differences were confirmed by Larson *et al.*, 1986, El-Naggar *et al.*, 1992, Barbour and Lilburn, 1995, Mandour *et al.*, 1996 and Sherif *et*

al., 1998. Strain difference in growth of commercial Japanese Quails and consequently growth traits, is often ascribed to stage of maturity (Moran *et al.*, 1978; Moran *et al.*, 1984). However, Blair *et al.*, 1989 also cite evidence for a Japanese Quail strain difference in growth composition that may influence nutrient requirement. In this respect, Bordas *et al.*, 1996 concluded that when egg laying lines were divergently selected for residual feed consumption and in spite of their differences in selection criteria, they remained genetically similar in egg production and body weight related traits.

Heterotic effect (H^1):

Estimates of direct (H^1) and individual or directional heterosis calculated in units (g) and percentages (%) for growth traits (*i.e.* BW, GW and GR) are presented in table 5. However, these traits showed generally highly significant ($P \leq 0.0001$; $P \leq 0.001$ or $P \leq 0.01$) negative direct heterosis except GR during 4-6 weeks of age at when H^1 was significantly ($P \leq 0.01$) positive. Similarly, Bahie El-Deen *et al.*, (1994) observed negative insignificant heterosis for BW at 6 weeks when they crossed two lines of quails, one selected for high BW at 6 weeks of age and the other was selected for high egg production. On the other hand, Gerken *et al.*, (1988) in diallel crosses among two randombred control lines and a line selected for a large body size, reported that heterosis was not significant for BW from 25 to 49 days of age.

Percentage of BW direct heterosis ($H^1\%$) ranged between -5.39 and -1.41 %. However absolute value of $H^1\%$ generally decreases as birds advance in age till the 4th weeks of age and started increasing thereafter. These results of direct and individual or directional heterosis following the crossing of quail lines selected short-term for high growth and egg production selection indices give the impression that they are dependent on age.

In this respect, Baik and Marks (1993) reported that heterosis declined from 10% at the first weeks to 6% at the 6th weeks of age. Also, Marks (1995) showed that quail gained high percentage heterosis of 20 to 30% for the first weeks body weight and declined linearly 5 to 10% at 4 wks when fed 28 and 24% CP diets. Contrariwise, when fed a low-CP (20%) diet, heterosis values were low initially and remained stable or increased across age. It was concluded that heterosis is present for body weight in Japanese quail following the crossing of lines selected long-term for high body weight, but it is dependent on both environment and age.

Effects of Crossing Two Japanese-Quail-Lines Selected

Table 3: Least squares means, (\pm standard errors, SE) of various factors affecting body weight, g. (BW), gain in weight, g. (GW) and Growth rate, % (GR) of Japanese Quail from hatch till 6 weeks of age.

	Body weight / Age per weeks					
	At hatch	2 wks	4 wks	6 wks		
Overall Mean	8.47 \pm 0.01	56.55 \pm 0.21	101.34 \pm 0.26	145.28 \pm 0.46		
Straight-Bred lines:						
Meat line (M)	8.56 \pm 0.01	58.05 \pm 0.32	104.36 \pm 0.39	148.62 \pm 0.70		
Egg line (E)	8.51 \pm 0.01	57.23 \pm 0.32	103.93 \pm 0.39	148.46 \pm 0.70		
Overall (Lines)	8.53 \pm 0.01	57.64 \pm 0.23	104.14 \pm 0.28	148.54 \pm 0.49		
Cross-Bred:						
M X E	8.38 \pm 0.02	55.61 \pm 0.50	98.23 \pm 0.61	141.40 \pm 1.08		
E X M	8.44 \pm 0.02	55.31 \pm 0.53	98.82 \pm 0.63	142.62 \pm 1.13		
Overall (Crosses)	8.41 \pm 0.02	55.46 \pm 0.36	98.53 \pm 0.44	142.01 \pm 0.78		
Hatch X sex combination (HS):						
1 st Hatch (Males)	8.39 \pm 0.02	54.14 \pm 0.51	97.73 \pm 0.62	139.28 \pm 1.11		
2 nd Hatch (Females)	8.52 \pm 0.02	57.96 \pm 0.52	103.67 \pm 0.62	149.71 \pm 1.11		
2 nd Hatch (Males)	8.42 \pm 0.02	55.75 \pm 0.49	99.61 \pm 0.59	141.16 \pm 1.05		
2 nd Hatch (Females)	8.52 \pm 0.02	59.43 \pm 0.54	104.64 \pm 0.66	152.27 \pm 1.17		
3 rd Hatch (Males)	8.45 \pm 0.02	54.22 \pm 0.53	98.87 \pm 0.64	140.23 \pm 1.13		
2 nd Hatch (Females)	8.54 \pm 0.03	57.80 \pm 0.56	103.50 \pm 0.68	149.00 \pm 1.21		
	Gain in weight / Age periods per weeks					
	0-2	0-4	0-6	2-4	2-6	4-6
Overall Mean	48.08 \pm 0.21	92.86 \pm 0.25	136.80 \pm 0.49	44.79 \pm 0.14	88.73 \pm 0.32	43.94 \pm 0.27
Straight-Bred lines:						
Meat line (M)	49.50 \pm 0.31	95.81 \pm 0.38	140.07 \pm 0.69	46.31 \pm 0.21	90.57 \pm 0.48	44.26 \pm 0.41
Egg line (E)	48.72 \pm 0.31	95.42 \pm 0.38	139.95 \pm 0.69	46.70 \pm 0.21	91.23 \pm 0.48	44.63 \pm 0.41
Overall (Lines)	49.11 \pm 0.22	95.61 \pm 0.27	140.00 \pm 0.49	46.50 \pm 0.15	90.90 \pm 0.34	44.39 \pm 0.29
Cross-Bred:						
M X E	47.23 \pm 0.49	89.85 \pm 0.59	133.02 \pm 1.07	42.62 \pm 0.32	85.79 \pm 0.75	43.17 \pm 0.61
E X M	46.87 \pm 0.51	90.38 \pm 0.62	134.18 \pm 1.12	43.51 \pm 0.34	87.32 \pm 0.78	43.81 \pm 0.67
Overall (Crosses)	47.05 \pm 0.35	90.11 \pm 0.43	133.60 \pm 0.77	43.07 \pm 0.23	86.55 \pm 0.54	43.49 \pm 0.46
Hatch X sex combination (HS):						
1 st Hatch (Males)	45.75 \pm 0.50	89.34 \pm 0.61	130.70 \pm 1.10	43.59 \pm 0.33	85.15 \pm 0.77	41.55 \pm 0.66
2 nd Hatch (Females)	49.45 \pm 0.50	95.15 \pm 0.61	141.19 \pm 1.10	45.70 \pm 0.33	91.75 \pm 0.77	46.04 \pm 0.65
2 nd Hatch (Males)	47.33 \pm 0.47	91.18 \pm 0.58	132.74 \pm 1.04	43.85 \pm 0.31	85.41 \pm 0.73	41.55 \pm 0.62
2 nd Hatch (Females)	50.91 \pm 0.53	96.12 \pm 0.64	143.75 \pm 1.15	45.21 \pm 0.35	92.85 \pm 0.80	47.63 \pm 0.69
3 rd Hatch (Males)	45.77 \pm 0.51	90.42 \pm 0.62	131.79 \pm 1.12	44.65 \pm 0.34	86.01 \pm 0.78	41.36 \pm 0.67
2 nd Hatch (Females)	49.26 \pm 0.55	94.96 \pm 0.67	140.46 \pm 1.20	45.70 \pm 0.36	91.20 \pm 0.84	45.50 \pm 0.72
	Growth rate / Age periods per weeks					
	0-2	0-4	0-6	2-4	2-6	4-6
Overall Mean	73.55 \pm 0.07	84.44 \pm 0.03	88.84 \pm 0.03	28.59 \pm 0.10	44.02 \pm 0.09	17.67 \pm 0.08
Straight-Bred lines:						
Meat line (M)	73.98 \pm 0.11	84.76 \pm 0.05	88.99 \pm 0.05	28.74 \pm 0.14	43.87 \pm 0.14	17.33 \pm 0.11
Egg line (E)	73.80 \pm 0.11	84.76 \pm 0.05	89.04 \pm 0.05	29.16 \pm 0.14	44.39 \pm 0.14	17.50 \pm 0.12
Overall (Lines)	73.89 \pm 0.08	84.76 \pm 0.04	89.01 \pm 0.03	28.95 \pm 0.10	44.13 \pm 0.10	17.42 \pm 0.08
Cross-Bred:						
M X E	73.37 \pm 0.17	84.12 \pm 0.08	88.64 \pm 0.05	27.94 \pm 0.22	43.57 \pm 0.21	17.82 \pm 0.18
E X M	73.06 \pm 0.18	84.11 \pm 0.08	88.68 \pm 0.05	28.51 \pm 0.23	44.26 \pm 0.22	18.04 \pm 0.19
Overall (Crosses)	73.22 \pm 0.12	84.12 \pm 0.06	88.66 \pm 0.03	28.22 \pm 0.16	43.91 \pm 0.15	17.93 \pm 0.13
Hatch X sex combination (HS):						
1 st Hatch (Males)	72.76 \pm 0.17	84.02 \pm 0.05	88.48 \pm 0.07	28.89 \pm 0.23	44.09 \pm 0.21	17.43 \pm 0.19
2 nd Hatch (Females)	74.06 \pm 0.17	84.71 \pm 0.05	89.12 \pm 0.07	29.47 \pm 0.23	44.24 \pm 0.22	18.07 \pm 0.19
2 nd Hatch (Males)	73.39 \pm 0.16	84.30 \pm 0.05	88.61 \pm 0.07	28.45 \pm 0.22	43.44 \pm 0.21	17.13 \pm 0.18
2 nd Hatch (Females)	74.60 \pm 0.18	84.85 \pm 0.05	89.27 \pm 0.08	29.74 \pm 0.24	43.85 \pm 0.23	18.31 \pm 0.20
3 rd Hatch (Males)	72.65 \pm 0.18	84.12 \pm 0.05	88.49 \pm 0.07	28.36 \pm 0.23	44.28 \pm 0.22	17.18 \pm 0.19
2 nd Hatch (Females)	73.87 \pm 0.19	84.64 \pm 0.05	89.03 \pm 0.08	29.57 \pm 0.25	44.21 \pm 0.24	17.91 \pm 0.20

Table 4: Linear function, (\pm standard errors, SE) of straight-bred differences and crossbreeding effects concerning body weight, g. (BW), gain in weight, g. (GW) and Growth rate, % (GR) of Japanese Quail from hatch till 6 weeks of age.

Crossbreeding effect		Body weight (BW) / Age per weeks					
		At hatch	2 wk.	4 wk.	6 wk.		
Straight-Bred differences		*	ns	ns	ns		
Meat (M) vs. Egg line (E)		0.04 \pm 0.02	0.82 \pm 0.46	0.43 \pm 0.55	0.16 \pm 0.98		
Direct Heterosis (H ^d)		****	****	****	****		
Value (g.)		-0.12 \pm 0.02	-2.18 \pm 0.43	-5.61 \pm 0.52	-6.53 \pm 0.92		
Percentage (%)		-1.41	-3.78	-5.39	-4.40		
Individual Heterosis (H ⁱ)		***	***	***	***		
M X E	Value (g.)	-0.15 \pm 0.03	-2.03 \pm 0.55	-5.91 \pm 0.67	-7.14 \pm 1.19		
	(%)	-1.76	-3.52	-5.68	-4.81		
E X M	Value (g.)	-0.09 \pm 0.03	-2.33 \pm 0.57	-5.33 \pm 0.69	-5.91 \pm 1.23		
	(%)	-1.06	-4.04	-5.12	-3.98		
Direct additive (G ^d)		ns	ns	ns	ns		
Meat type (M)		-0.01 \pm 0.02ns	0.56 \pm 0.43ns	-0.08 \pm 0.52ns	-0.53 \pm 0.92ns		
Maternal additive (G ^m)		ns	ns	ns	ns		
Meat type (M)		0.05 \pm 0.03ns	-0.30 \pm 0.73ns	0.59 \pm 0.88ns	1.23 \pm 1.56ns		
Crossbreeding effect		Gain in weight (GW) / Age period per weeks					
		0-2	0-4	0-6	2-4	2-6	4-6
Straight-Bred differences		ns	ns	ns	ns	ns	ns
Meat (M) vs. Egg line (E)		0.77 \pm 0.44	0.39 \pm 0.54	0.12 \pm 0.97	-0.39 \pm 0.29	-0.66 \pm 0.68	-0.27 \pm 0.58
Direct Heterosis (H ^d)		***	***	***	***	***	ns
Value (g.)		-2.06 \pm 0.42	-5.50 \pm 0.51	-6.41 \pm 0.91	-3.44 \pm 0.27	-4.34 \pm 0.64	-0.91 \pm 0.55
Percentage (%)		-4.19	-5.75	-4.58	-7.40	-4.77	-2.05
Individual Heterosis (H ⁱ)		***	***	***	***	***	ns
M X E	Value (g.)	-1.88 \pm 0.54	-5.76 \pm 0.65	-6.99 \pm 1.17	-3.88 \pm 0.36	-5.11 \pm 0.82	-1.23 \pm 0.70
	(%)	-3.83	-6.02	-4.99	-8.34	-5.62	-2.77
E X M	Value (g.)	-2.24 \pm 0.56	-5.24 \pm 0.67	-5.82 \pm 1.22	-2.99 \pm 0.37	-3.58 \pm 0.85	-0.59 \pm 0.73
	(%)	-4.56	-5.48	-4.16	-6.43	-3.94	-1.33
Direct additive (G ^d)		ns	ns	ns	*	ns	ns
Meat type (M)		0.57 \pm 0.42	-0.07 \pm 0.51	-0.52 \pm 0.91	-0.64 \pm 0.28	1.09 \pm 0.64	-0.45 \pm 0.55
Maternal additive (G ^m)		ns	ns	ns	ns	ns	ns
Meat type (M)		-0.36 \pm 0.70	0.53 \pm 0.86	1.17 \pm 1.55	0.89 \pm 0.47	1.53 \pm 1.08	0.64 \pm 0.93
Crossbreeding effect		Growth Rate (GR) / Age period per weeks					
		0-2	0-4	0-6	2-4	2-6	4-6
Straight-Bred differences		ns	ns	ns	*	**	ns
Meat (M) vs. Egg line (E)		0.19 \pm 0.15	-0.01 \pm 0.07	-0.04 \pm 0.06	-0.42 \pm 0.20	-0.52 \pm 0.19	-0.17 \pm 0.16
Direct Heterosis (H ^d)		***	***	***	****	ns	**
Value (g.)		-0.67 \pm 0.14	-0.64 \pm 0.07	-0.36 \pm 0.06	-0.73 \pm 0.19	-0.21 \pm 0.18	0.51 \pm 0.16
Percentage (%)		-0.91	-0.76	-0.40	-2.52	-0.48	2.93
Individual Heterosis (H ⁱ)		**	***	***	***	*	*
M X E	Value (g.)	-0.52 \pm 0.18	-0.63 \pm 0.09	-0.38 \pm 0.08	-1.01 \pm 0.24	-0.56 \pm 0.23	0.41 \pm 0.20
	(%)	-0.70	-0.74	-0.43	-3.49	-1.27	2.35
E X M	Value (g.)	-0.83 \pm 0.19	-0.64 \pm 0.09	-0.33 \pm 0.08	-0.44 \pm 0.25	0.13 \pm 0.24	0.62 \pm 0.21
	(%)	-1.12	-0.76	-0.37	-1.52	0.29	3.56
Direct additive (G ^d)		ns	ns	ns	**	***	ns
Meat type (M)		0.24 \pm 0.14	0.00 \pm 0.07	-0.04 \pm 0.06	-0.50 \pm 0.19	-0.61 \pm 0.18	-0.19 \pm 0.16
Maternal additive (G ^m)		ns	ns	ns	ns	*	ns
Meat type (M)		-0.31 \pm 0.24	-0.01 \pm 0.11	0.05 \pm 0.10	0.57 \pm 0.32	0.69 \pm 0.31	0.21 \pm 0.26

ns : not significant at $P \leq 0.05$; * significant at $P \leq 0.05$; ** significant at $P \leq 0.01$; *** significant at $P \leq 0.001$; **** significant at $P \leq 0.0001$.

Heterosis or hybrid vigor for a certain character, is exist when the average performance of crossbred progeny is superior to the average performance of the two parents. The amount of heterosis can vary practically, depending on the environment and on the populations being crossed. Theoretically, the magnitude of heterosis is inversely related to the degree of genetic resemblance between parental populations (Willham and Pollak, 1985) and it is expected to be proportional to the degree of heterozygosity of the crosses (Sheridan, 1981 and Hill, 1982). This is of major genetic importance for any long-term breeding program that is undertaken to design a production strategy involving complex multibreed individuals. Various types of heterosis are recognized, including parental heterosis (either maternal or paternal), referring to the performance of animals as parents, and individual or directional heterosis, referring to the non-parental heterosis.

Howbeit, negative direct heterosis, if any, might be attributable to directional dominance of genes affecting these traits. Differences in the direction and magnitude of specific cross heterotic effects might lead us to assume that at least a considerable part of genes affecting these traits lies on the sex chromosomes. In this respect, Falconer (1989) showed that a cross between two base populations would show heterosis if they diverge in the frequency of genes affecting a given trait. The same author also added that the negative sign of heterosis could be attributed in some cases to the nature of the measurement (*i.e.* if the trait is expressed in another way such as the reciprocal of the present the heterosis would be positive in sign).

Direct additive effect (G^i):

Crossing not only takes advantage of characters with considerable non-additive genetic variations (*i.e.* dominance and epistasis), but also exploits differences in additive effects (*i.e.* differences in average performance between populations as a deviation from the overall mean) between populations (Ahmed, 2003). On the level of loci responsible for a given trait, complementarity between additive effect of genes occupying these loci play an important role in the manifestation of G^i .

Contrasts of G^i on body weight at most ages studied were negative, except at 2nd week of age, and insignificant ($P \leq 0.05$). Sire line linear contrasts indicate that E sired quails were significantly superior in GW during 2-4 weeks ($P \leq 0.05$) as well as GR during 2-4 ($P \leq 0.01$) and 2-6 ($P \leq 0.001$) weeks of age.

In a comparable crossbreeding experiment, similar results were found by Bahie El-Deen *et al.*,

(1998) who concluded that both additive and nonadditive genetic effects influenced growth traits of quails insignificantly. In contrast, Moritsu *et al.*, (1997) indicated that additive genetic variance estimated as the sire breed differences between divergently selected lines in growth traits was important.

It could be concluded that this relatively low and inclusive discrimination between the lines selected in this population of Japanese Quail could be due to the previous selection of BW it had been subjected for in previous generation. Also, it seems that using selection index for improving more than one trait is less effective, compared with individual selection for a single trait, to cause gene frequencies of involved loci to diverge, which in turn may reduce the degree of complementarity.

Maternal additive effect (G^m):

Maternal effect (G^m) consists mainly from additive maternal and cytoplasmic-inheritance. However, the maternal effect herein is conceivably confounded with the reciprocal effect (*i.e.* sex linkage) since it is determined as the difference between the two reciprocal crosses. Sex linkage as an effect, is due to additive effects of the genes concerned and carried on the sex chromosomes.

Denoting G^m in terms of complementarity effect, certain crosses may show much more G^m than others depending upon the extent to which the crossed populations differ in reproductive performance and in production characterers. Therefore, this type of effect relies on the direction of the crossing (Ahmed, 2003).

In the scope of the present data, results in table 5 demonstrated that G^m effect on all growth traits were not significant, except for GR at the age period 2-6 wk. However, no trend could be detected for the effect of G^m on the studied growth traits. These results may lead us to assume that both lines of the present study could be used as a dam-line and they are closely comparable considering their mothering ability. In other words, the two selected lines do not complement each other or aggregate the responsible genes, regarding maternal effect and reproductive efficiency of the studied traits.

Equivalent results were retrieved by Chahil *et al.*, (1975), who reported non-significant G^m on 5-week body weight in a 3 x 3 diallel cross of three random mating populations of quail. On the other hand, Baik and Marks (1993) obtained a significant maternal effect denoted as the significant reciprocal effects between the high- (HW) x low- (LW) body weight and LW x HW crosses (in a

crossing schema between lines of Japanese quail, divergently selected for 4-week BW). In this respect, Fairfull, 1990 reported that heterosis and maternal effects can importantly influence juvenile growth traits, but in opposition these effects are reported to be sporadic and less important to sex linkage by Barbato and Vasilatos-Younken, 1991.

However, reciprocal recurrent selection between these two selected lines could be of value in increasing the nicking ability between them and in our case increase their G^m .

Variance components (σ):

Variance components values (σ) and percentages (%) are presented in table 5 regarding the sire- (SB); dam-Breed (DB) and sire X dam interactions (SB X DB) as random effects. Analysis of variance (Table 2) revealed that SB and DB were rarely a significant source of variation for growth traits in the flock under consideration. However, SB X DB interactions was generally distinguished as an eminent cause of significant variation ($P \leq 0.0001$ or $P \leq 0.001$). Values of SB X DB variance components were between 2.999 to 13.611 % in BW and 0.144 to 10.675 % in GW and 0.207 to 17.910 % in GR. The later result reveal that, apart from the error variance component which was accountable for 81.578 to 99.793 of the overall variance, SB X DB variance was the greatest component and may suggest a notable non-additive genetic association between the two herds being crossed with regard to growth traits. Nevertheless, sire breed variance component (as a descriptive measure of additive

genetic variance) is awfully weak and inadequate ranging from 0.000 to 0.034; 0.000 to 0.704 and 0.000 to 0.512% in BW; GW and GR; respectively.

As regard to dam-breed variance component (as a measure of additive genetic variance confounded with maternal effects) it is also extremely insubstantial ranging from 0.000 to 0.694 and 0.000 to 0.000 and 0.000 to 0.018% in BW; GW and GR; respectively. The profile that can be extracted from the previous results is that, selection for the non-additive variance is the procedure of choice if the selection goal is to improve growth traits in the herd of quail under consideration. Therefore, reciprocal recurrent selection is needed to increase the exploitation of such a component.

Genetic distance index (D):

Effects of short- and long-term selection on the allocation of resources under different environmental settings continued to receive considerable emphasis in research all over the world. Intense selection can create a genetic stress which may be compounded by environmental stressors or alleviated, in part, through crossing. Skeletal and metabolic disorders and ability to respond to pathogenic challenges, issues of economic and biological importance in both intensive and extensive production of poultry, may naturally have impacts on growth traits. Fundamental to such thinking is that genetic predisposition for immune response and nongenetic factors, vaccination programs, and biosecurity measures, are important in the

Table 5. Variance components (Values and percentages) of random effects of Breed of sire (BS); Breed of dam (DS); BS X BD interaction and the remainder for body weight (BW); Gain in weight (GN) and growth rate (GR) of Japanese quail from hatch till 6 wk. of age.

Trait & Age	Breed of sire (BS)		Breed of dam (DS)		BS X BD		Error or Remainder		Total Value
	Value	%	Value	%	Value	%	Value	%	
Body weight:									
At hatch	0.000	0.000	0.001	0.001	0.007	4.301	0.136	0.001	0.144
2 wks.	0.023	0.004	0.000	0.000	2.031	2.999	65.661	0.000	70.724
2 wks.	0.000	0.000	0.043	0.009	15.111	13.611	95.866	0.000	124.630
2 wks.	0.000	0.000	0.000	0.000	19.942	6.160	303.809	0.000	330.751
Gain in weight:									
0-2 wks.	0.014	0.106	0.000	0.000	0.190	2.016	7.341	0.000	7.537
0-4 wks.	0.000	0.000	0.000	0.000	0.196	10.675	1.640	0.000	11.411
0-6 wks.	0.000	0.000	0.000	0.000	0.059	4.307	1.286	0.000	5.642
2-4 wks.	0.093	0.704	0.000	0.000	0.286	2.169	12.829	0.000	15.276
2-6 wks.	0.156	1.323	0.000	0.000	0.017	0.144	11.614	0.000	12.797
4-6 wks.	0.007	0.081	0.000	0.000	0.119	1.372	8.549	0.000	9.929
Growth rate:									
0-2 wks.	0.033	0.052	0.000	0.000	1.801	2.839	61.603	0.000	65.435
0-4 wks.	0.000	0.000	0.019	0.018	14.473	10.633	91.671	0.000	116.761
0-6 wks.	0.000	0.000	0.000	0.000	19.207	0.000	296.467	0.000	315.674
2-4 wks.	0.170	0.512	0.000	0.000	5.951	17.910	27.106	0.000	33.967
2-6 wks.	0.471	0.305	0.000	0.000	9.135	6.925	144.582	0.000	154.642
4-6 wks.	0.000	0.000	0.000	0.000	0.221	0.207	106.362	0.000	106.789

Negative variance component estimates are set to be zero.

endeavor to protect chickens from pathogens in addition to reduce skeletal and metabolic disorders.

Selection for growth traits resulted in positive correlated responses in feed intake and carcass fat and negative associations with some reproductive and immunological traits. It appears that selection for juvenile body weight enhances rapid development of vital organs such as the gonads and liver which may be essential to subsequent demands required for accelerating growth of bone and muscle (Baker *et al.*, 1998 and Siegel, 1998). Selection for body weight resulted in a positive correlated response in hematocrits (Price *et al.*, 1998) which may contribute to ascites.

Genetic distance (D) reflects the genetic relationship between populations (Hartl and Clark, 1989; Kuhnlein *et al.*, 1989 and Siegel *et al.*, 1992). It measures to what extent are two distinct populations are genetically situated apart from each other in respect to a given traits.

Genetic distance indices presented in table 6 revealed that, by sex comparisons, D of body weight (BW) and gain in weight (GW) were generally greater in case of females compared with males. However, in case of growth rate (GR) there is no detectable trend for D figures as affected by sex. This sexual dimorphism could be due to that females have different response to selection compared with males which resulted in the emphasis of farther genetic difference index. The results of GR are likely to be more complicated since it is a function of both BW and GW as well as it was not a common practice for selection (though it was for the meat line). It seems also that males have different body composition and periority of organs development which in turn have its consequence on the genes and metabolic pathways involved. Also D values reported herein may reveal that females may have a greater response to selection compared to males. In this respect El-Gendy, 2000 reported such sexual dimorphism with males retained the greatest D values in ckickens. The same author also reported that the greater response to selection in males may explain such results.

Based on Hatch, D was on average getting larger as hatch rank progressing. Since selection was made on later ages (28 days for the meat line and at sexual maturity for the egg line), D values was greater at later ages compared to that at ealier ones. These results may reveal that there is a consistent affiliation between the genetic distance and the selection practices performed. However, using different selection criteria may affect the

simplicity of the lines divergence which consecutively complicate the interpretations and elucidation of the results of D values. Bordas *et al.*, 1996 concluded that when egg laying lines were divergently selected for residual feed consumption and in spite of their differences in selection criteria, they remained genetically similar in egg production and body weight related traits.

However, the lack of significant differences between the pure lines (Table 4) may explain the deficiency of genetic divergence between lines (negative D values). In this respect Siegel *et al.*, 1992 and Smith *et al.*, 1996 concluded that intra-species or substrain genetic distances were low compared to larger interspecies or between strains genetic distances. They reported that D between two strains of Single Comb White Leghorn previously shared a common genetic background was 1.25 while it was 3.12 between a White Leghorn and a New Hampshire substrain of chickens.

Conclusion:

There was no evidence of positive heterosis, and reciprocal or maternal effects were negligible due to crossing between the two short-term selected quail lines for high growth and egg production selection indicies. The two selected lines do not complement each other or aggregate the responsible genes, regarding direct and maternal additive effects of the studied traits. This relatively low and inexclusive discrimination between the selected-lines in this population of Japanese quail could be due to the previous selection of BW it had been subjected for in previous generation. This previous selection could probably consumed large proportion of the additive variance. Another explanation is that the short-term selection (*i.e.* 7 generation) for high growth and egg production selection indicies on the same base population did not generate sufficient diversity in the selected lines. The two traits used as selection critorian (*i.e.* high growth and egg production), are composite traits which may have many common genetic factors especially those of metabolic effeciency and the selection was performed in the same direction. However, reciprocal recurrent selection between these two selected lines could be of value in increasing the nicking ability beween them. The profile that can be extracted from the previous results is that, selection for the non-additive variance is the procedure of choise if the selection goal is to improve growth traits in the herd of quail under consideration. Therefore, reciprocal recurrent selection is needed to increase the exploitation of such a component.

Table 6: Indices of genetic distance (D^S) between two lines of Japanese Quail selected short-term for egg and meat production as affected by different factors with regard to body weight, g. (BW), gain in weight, g. (GW) and Growth rate, % (GR) traits of from hatch till 6 weeks of age.

Factor	Body weight (BW) / age per weeks					
	At hatch	2 wks	4 wks	6 wks		
Overall	0.0134	0.0329	0.0524	0.0413		
Sex:						
Males	0.0120	0.0155	0.0520	0.0350		
Females	0.0163	0.0587	0.0581	0.0554		
Hatches						
1st	0.0085	0.0263	0.0403	0.0290		
2nd	0.0140	0.0104	0.0425	0.0356		
3rd	0.0179	0.0664	0.0753	0.0598		
Sex X Hatch						
1st Hatch Males	0.0099	0.0073	0.0437	0.0201		
2nd Hatch Males	0.0135	0.0049	0.0463	0.0415		
3rd Hatch Males	0.0119	0.0394	0.0684	0.0421		
1st Hatch Females	0.0099	0.0568	0.0473	0.0497		
1st Hatch Females	0.0146	0.0201	0.0408	0.0312		
1st Hatch Females	0.0255	0.1004	0.0860	0.0834		
Factor	Gain in weight (GW) / age periods per weeks					
	0-2	0-4	0-6	2-4	2-6	4-6
Overall	0.0364	0.0559	0.0431	0.0769	0.0467	0.0158
Sex:						
Males	0.0162	0.0558	0.0365	0.0975	0.0476	-0.0054
Females	0.0659	0.0618	0.0578	0.0573	0.0533	0.0494
Hatches						
1st	0.0295	0.0432	0.0303	0.0578	0.0307	0.0030
2nd	0.0098	0.0451	0.0370	0.0840	0.0520	0.0198
3rd	0.0751	0.0806	0.0624	0.0864	0.0556	0.0234
Sex X Hatch						
1st Hatch Males	0.0069	0.0469	0.0208	0.0889	0.0282	-0.0353
2nd Hatch Males	0.0034	0.0494	0.0433	0.0990	0.0654	0.0300
3rd Hatch Males	0.0445	0.0737	0.0440	0.1036	0.0437	-0.0208
1st Hatch Females	0.0648	0.0507	0.0521	0.0354	0.0452	0.0550
2nd Hatch Females	0.0210	0.0431	0.0322	0.0680	0.0383	0.0101
3rd Hatch Females	0.1134	0.0915	0.0869	0.0679	0.0726	0.0774
Factor	Growth rate (GR) / age periods per weeks					
	0-2	0-4	0-6	2-4	2-6	4-6
Overall	0.0029	0.0074	0.0031	0.0549	0.0162	-0.0478
Sex:						
Males	0.0148	0.0077	0.0050	-0.0031	-0.0039	-0.0062
Females	0.0076	0.0072	0.0037	0.0295	0.0067	-0.0306
Hatches						
1st	0.0070	0.0062	0.0027	0.0219	0.0009	-0.0345
2nd	0.0004	0.0052	0.0032	0.0498	0.0243	-0.0121
3rd	0.0165	0.0103	0.0050	0.0131	-0.0079	-0.0472
Sex X Hatch						
1st Hatch Males	0.0014	0.0068	0.0018	0.0556	0.0096	-0.0680
2nd Hatch Males	-0.0011	0.0058	0.0038	0.0625	0.0334	-0.0084
3rd Hatch Males	0.0102	0.0101	0.0037	0.0430	0.0003	-0.0771
1st Hatch Females	0.0159	0.0069	0.0049	-0.0166	-0.0080	0.0041
2nd Hatch Females	0.0034	0.0050	0.0028	0.0326	0.0121	-0.0173
3rd Hatch Females	0.0250	0.0108	0.0070	-0.0252	-0.0178	-0.0101

$D^S = \frac{1}{2} \ln \left[\frac{[0.5 * (p_{11} + p_{22})] + [0.5 * (p_{12} + p_{21})]}{[0.5 * (p_{11} + p_{22})]} \right]$ as reported by Nei, 1978 and Hartl and Clark, 1989.

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تأثير التهجين بين خطين من السمان الياباني منتخبة سبعة أجيال لإنتاج اللحم أو البيض على صفات النمو

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استخدمت بيانات ١٧٧٩ طائر مكونة من ١٢٧٢ سلالات نقية و ٥٠٦ هجن نتجت من خطين من السمان الياباني منتخبة لسرعة النمو والبيض على الترتيب والهجن العكسية منهما. هدفت الدراسة إلى تقييم تأثيرات قوة الهجين والوراثة للتهجين (التجمعي المباشر والأمي المضاف) على صفات النمو التي شملت أوزان الجسم كل أسبوعين الزيادة في وزن الجسم وسرعة النمو من الفقس وحتى ٦ أسابيع من العمر.

أظهرت اختبارات المعنوية أن تأثير مجاميع التربية كان معنوياً على أغلب الصفات المدروسة ما عدا وسرعة النمو خلال الفترة من ٤-٦ أسابيع. تأثير التوافق بين ترتيب الفقس والجنس كان معنوياً على الصفات المدروسة ما عدا وزن الجسم عند ٦ أسابيع. ولم تظهر سلالة الأب أو الأم أي تأثير معنوي على صفات النمو ما عدا سلالة الأم على وزن الجسم عند الفقس و سلالة الأب على الزيادة في وزن الجسم خلال الفترة من ٢-٤ أسابيع وسرعة النمو خلال الفترة من ٢-٤ و ٢-٦ أسابيع من العمر. وبالنسبة للتداخل بين سلالاتي الأب والأم فقد كان تأثيرها عالى المعنوية على الاختلافات في أغلب الصفات المدروسة ما عدا الزيادة في وزن الجسم خلال الفترة من ٤-٦ أسابيع وسرعة النمو خلال الفترة من ٢-٦ أسابيع من العمر.

وقد كانت قوة الهجين سالبة وعالية المعنوية على أغلب الصفات المدروسة ما عدا سرعة النمو خلال الفترة من ٤-٦ أسابيع من العمر حيث كانت كوجبة ومعنوية. وبالنسبة للتأثيرين التجمعي المباشر والأمي المضيف فقد كانا في الغالب غير معنويين على أغلب الصفات المدروسة ما عدا التأثير التجمعي المباشر على الزيادة في وزن الجسم خلال الفترة من ٢-٤ أسابيع من العمر في صالح خط البيض وكذا التأثير الأمي المضيف على سرعة النمو خلال الفترة من ٢-٤ و ٤-٦ أسابيع من العمر في صالح الخط سريع النمو. من نتائج التهجين السابقة يمكن التوصية بأن استخدام دليل الانتخاب لسبعة أجيال كان غير كاف لتغيير الخلفية الوراثية للخطين محل الدراسة وأن استخدام خطي البيض واللحم الحاليين ما زال في حاجة إلى قدر من الانتخاب الدورى المتبادل لتحقيق الهدف من استخدامهما في تحسين صفات النمو.